b.) Remarks

Claims 1-3, 5 and 6 have been amended in order to recite the present invention with the specificity required by statute. No new matter has been added.

Claims 1 and 6 are objected for comprising non-elected subject matter (SEQ ID NO: 5, 7, 9, 11, 13 and 15). In response, claims 1 and 6 have above been amended to delete the non-elected subject matter. This objection is therefore overcome.

The Examiner also objected to the language of the claims for various grammatical reasons. In response, to reduce the issues, claims 1-3, 5 and 6 have been amended in conformity with the Examiner's kind suggestions. Accordingly, this objection is mooted.

The Examiner objects to claim 7 as being a substantial duplicate of claim 3. (In this regard, Applicants understand the Examiner intended to specify claim 5, not claim 3.) In response, claim 7 has been cancelled. Accordingly, this objection is mooted as well.

Claims 1-3 and 5-15 remain rejected under 35 U.S.C. §112, first and second paragraphs, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventors had possession of the claimed invention when the application was filed, as well as because the Examiner states practicing the scope of the claims is not enabled.

Initially, in support of the rejections, the Examiner notes "a nucleotide sequence complementary" means a fragment of any size which is complementary to SEQ ID NO:3. Although Applicants respectfully submit such is not at all what the claims

literally recite, the Examiner's comment is above mooted by amending the claims to recite "full length".

As to the Examiner's technical analyses provided in the paragraph bridging pages 4-5, Applicants respectfully wish to explain the written description requirement is designed to evaluate what the specification means to one of ordinary skill in the art. In that regard, those of ordinary skill in this art are aware that if the calculated identity of the hybridizable sequence is 69.8%, the microorganism is very unlikely to provide a gene that encodes a protein having NADH-II dehydrogenase activity. Therefore, since 69.8% is sufficient for specifying the activity of a novel protein, one skilled in this art can easily obtain the gene encoding NADH-II dehydrogenase from the genomic DNA of the microorganism by the hybridization condition recited in claim 1. While random irrelevant genes may be isolated by such hybridization process, it is very easy to identify the gene encoding NADH-II dehydrogenase without undue experimentation because genes which have 69.8% identity with the gene of NADH-II dehydrogenase are few.

Claims 1-3, 6, 8-10, 14 and 15 remain rejected under 35 U.S.C. §103(a) by Bott (*J. Biotechnol.* (2003) 129-53) in view of Molenaar (*J. Bact.* (2000) 6884-91), Hollander (*Appl. Microbiol. Biotechnol.*, Vol. 42 (1994) 508-15) and Nakagawa (U.S. Patent Publication No. 2002/0197605). Claims 11-13 are rejected under 35 U.S.C. §103(a) by Bott in view of Molenaar, Hollander and Nakagawa.

The Examiner's technical analyses in support of the rejection are provided at pages 15-18 of the Office Action. The salient feature of the rejection is found bridging pages 15-16:

> as explained in the 103(a) rejection above Bott et al and Molenaar et al teach that *C. glutamicum* comprises only one NADH dehydrogenase which is membrane bound NADH-II type whereas *E. coli* comprises both NADH-I and NADH-II... One of ordinary skill in the art would recognize that NADH-II dehydrogenase of *Corynebacterium glutamicum* is involved in amino acid production in *Corynebacterium glutamicum*.

Respectfully submitted, this is incorrect. Microorganisms such as *C. glutamicum* have many enzymes with the activity to oxidation of NADH (for instance, malate NAD oxidoreductase). Therefore, cannot be maintained that NADH-II dehydrogenase is necessarily involved in amino acid production, even if NADH-II dehydrogenase is only the NADH dehydrogenase in *C. glutamicum*.

The Examiner also states

> it is noted that (1) NADH-II dehydrogenase (100% identical to applicants SEQ ID NO:4) isolated from *Corynebacterium glutamicum* (only 27% sequence homology to that of *E. coli*) is not the same NADH-II of *E. coli*.

Respectfully submitted, this is incorrect as well. The name of an enzyme is determined based on the function of the enzyme, To this point, *C. glutamicum* NADH-II dehydrogenase fulfills a role with the same function as *E. coli* NADH-II dehydrogenase. Nakai does <u>not</u> note that NADH-II dehydrogenase isolated from *C. glutamicum* "is not same" NADH-II of *E. coli*; indeed, to the contrary Nakai specifically teaches *E. coli* has two kinds of terminal oxidases in its respiratory chain, named NDH-I (which has high energy efficiency) and NDH-II (which has low energy efficiency). *C. glutamicum* <u>also</u> has two kinds of terminal oxidases, one is an electron transfer pathway of high energy efficiency (SoxM type oxidase) and the other is an electron transfer pathway of low energy

efficiency (cytochrome bd type oxidase), see [0005] and [0006] of Nakai. Further, Nakai shows that *E. coli* in which (i) the respiratory chain pathway of high energy efficiency is enhanced, and (ii) the respiratory chain pathway of low energy efficiency is deficient can efficiently produce and accumulate amino acids.

Therefore, it is seen based on Nakai that (i) *C. glutamicum* has SoxM type oxidase, the respiratory chain pathway of high energy efficiency, and (ii) the SoxM type oxidase plays a role of a primary dehydrogenase, linked with central metabolism in *C. glutamicum*. It is also seen that (iii) *C. glutamicum* cytochrome bd type oxidase, the respiratory chain pathway of low energy efficiency, does not play a role in production of amino acids.

As also established on the record, the NADH-II of SEQ ID NO:4 is the respiratory chain pathway of low energy efficiency. Therefore NADH-II of Applicants' SEQ ID NO:4 has the same function as NADH-II of *E. coli*, as described in Nakai.

Because Nakai discloses that it is important to be deficient in NADH-II (e.g., the respiratory chain pathway of low energy efficiency) in *E. coli* for producing amino acids, the present invention, which produces amino acid by culturing *C. glutamicum* having amplified NADH-II, is plainly unobvious over the prior art.

Regarding a final formal matter, the Examiner did not acknowledge the Information Disclosure Statement filed June 26, 2009. Confirmation that the art cited therein has been considered and will appear on the face of any patent issuing herein is respectfully requested in the next Patent Office communication.

In view of the above amendments and remarks, Applicants submit that all of the Examiner's concerns are now overcome and the claims are now in allowable condition. Accordingly, reconsideration and allowance of this application is earnestly solicited.

Claims 1-3, 5, 6 and 8-15 remain presented for continued prosecution.

Applicants' undersigned attorney may be reached in our New York office by telephone at (212) 218-2100. All correspondence should continue to be directed to our below listed address.

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